

From: Gibbs, Terra
Sent: Monday, January 06, 2003 10:50 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

-) Could you please a regular search SEQ ID NO. 3
of Serial No. 10003354?
- 2) Also, please do an oligomer search of SEQ ID NO:3. Please limit the hits to 100 nucleotides or less.

**Terra Gibbs #79523
AU 1635
Mailbox 11E12
306-3221**

THANK YOU!

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: Bob B
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 1-13-03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM nucleic - nucleic search, using sw mode!

Run on: January 11, 2003, 02:33:22 ; Search time 119 Seconds
(without alignments)
9568.830 Million cell updates/sec

Title: US-10-003-354-3

Perfect score: 3713

Sequence: 1 attaacagggccgtgtttagg.....aaacttttaatgatgttattta 3713

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA*

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 1	17	0.5	42	4 US-09-171-425-2	Sequence 2, Appli
c 2	17	0.5	48	4 US-09-171-425-6	Sequence 6, Appli
c 3	17	0.5	48	4 US-09-171-425-7	Sequence 7, Appli
c 4	17	0.5	54	1 US-08-390-1044	Sequence 1044, AP
c 5	17	0.5	54	1 US-08-435-634-1044	Sequence 1044, AP
c 6	16	0.4	49	6 5516641-1	Patent No. 5516641
c 7	16	0.4	87	4 US-09-364-543-84	Sequence 84, Appli
c 8	16	0.4	97	1 US-08-182-175A-18	Sequence 48, Appli
c 9	16	0.4	97	1 US-08-474-633A-57	Sequence 57, Appli
c 10	16	0.4	97	4 US-08-823-771-57	Sequence 57, Appli
c 11	16	0.4	97	5 PCT-US92-05612-48	Sequence 48, Appli
c 12	15	0.4	18	5 US-08-890-960-64	Sequence 64, Appli
c 13	15	0.4	18	3 US-09-543-84	Sequence 84, Appli
c 14	15	0.4	18	3 US-09-032-994-64	Sequence 64, Appli
c 15	15	0.4	18	4 US-09-131-616-64	Sequence 64, Appli
c 16	15	0.4	19	2 US-08-656-306-3	Sequence 3, Appli
c 17	15	0.4	19	4 US-09-217-947-3	Sequence 3, Appli
c 18	15	0.4	21	3 US-08-851-550-23	Sequence 23, Appli
c 19	15	0.4	21	3 US-08-851-550-33	Sequence 33, Appli
c 20	15	0.4	22	1 US-08-379-078-64	Sequence 64, Appli
c 21	15	0.4	22	4 US-07-974-09C-2/2	Sequence 272, Appli
c 22	15	0.4	22	5 PCT-US93-00977-272	Sequence 272, Appli
c 23	15	0.4	32	1 US-09-150-766-8	Sequence 8, Appli
c 24	15	0.4	36	1 US-08-311-886C-424	Sequence 424, Appli
c 25	15	0.4	36	3 US-08-582-740-5	Sequence 5, Appli
c 26	15	0.4	36	4 US-09-109-829-5	Sequence 5, Appli
c 27	15	0.4	44	2 US-08-006-670A-59	Sequence 59, Appli

ALIGMENTS

RESULT 1
US-09-171-425-2/c
; Sequence 2, Application US/09171425A
; Patent No. 6465438
; GENERAL INFORMATION:
; APPLICANT: Schorr, Joachim
; APPLICANT: Baker, Henry J.
; APPLICANT: Smith, Bruce F.
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
; FILE REFERENCE: 08909/00/0001
; CURRENT APPLICATION NUMBER: US/09/171-425A
; CURRENT FILING DATE: 1998-10-19
; EARLIER APPLICATION NUMBER: PCT/EP97/01943
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO: 2
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotides

RESULT 2
US-09-171-425-2/c
; Sequence 6, Application US/09171425A
; Patent No. 6465438
; GENERAL INFORMATION:
; APPLICANT: Schorr, Joachim
; APPLICANT: Baker, Henry J.
; APPLICANT: Smith, Bruce F.
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
; FILE REFERENCE: 08909/00/0001
; CURRENT APPLICATION NUMBER: US/09/171-425A
; CURRENT FILING DATE: 1998-10-19
; EARLIER APPLICATION NUMBER: PCT/EP97/01943
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO: 2
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotides

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; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetically generated oligonucleotides
; US-09-171-425-6

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2562 CCAGCTTCTCTCTCTCT 2578
Db 47 CCAGCTTCTCTCTCTCT 31

RESULT 3
US-09-171-425-7
Sequence 7, Application US/09171425A
; Patent No. 6445438
; GENERAL INFORMATION:
; APPLICANT: Schorr, Joachim
; APPLICANT: Baker, Henry J.
; APPLICANT: Smith, Bruce F.
; TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
; FILE REFERENCE: 08909/030301
; CURRENT APPLICATION NUMBER: US/09/171,425A
; CURRENT FILING DATE: 1998-10-19
; EARLIER APPLICATION NUMBER: PCT/EP97/01943
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Synthetically generated oligonucleotides
; US-09-171-425-7

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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 47 CCAGCTTCTCTCTCTCT 31

RESULT 4
US-08-390-850-1044
; Sequence 1044, Application US/08435634
; Patent No. 5731293
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 56125Member 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32, 327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 1044:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base Pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-390-850-1044

Query Match 0.5%; Score 17; DB 1; Length 54;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3286 TCAGGGAAAGAAGGGGG 3302
Db 1 UCAGGGAAAGAAGGGGG 17

RESULT 5
US-08-435-634-1044
; Sequence 1044, Application US/08435634
; Patent No. 5731293
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 56125Member 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32, 327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 1044:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 base Pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-390-850-1044

Query Match 0.5%; Score 17; DB 1; Length 54;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3286 TCAGGGAAAGAAGGGGG 3302
Db 1 UCAGGGAAAGAAGGGGG 17

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CURRENT FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO: 84
 LENGTH: 87
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial sequence: Synthetic
 Sequence: Description: Sequence with defined structure containing
 feature:
 NAME/KEY: modified_base
 LOCATION: (1)..(87)
 OTHER INFORMATION: All pyrimidines are 2' F.
 US-09-364-543-84

Query Match 0 4%; Score 16; DB 4; Length 87;
 Best Local Similarity 75.0%; Pred. No. 4.2e+02;
 Matches 4; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 US-08-182-175A-48/C
 Sequence 48, Application US/08182175A
 Patent No. 5559223

GENERAL INFORMATION:
 APPLICANT: Saverio Carl Falco
 APPLICANT: Sharon J. Keefer
 APPLICANT: Janet A. Rice
 TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: E.I. du Pont de Nemours and Company
 STREET: 1007 Market Street
 CITY: Wilmington
 STATE: Delaware
 COUNTRY: USA
 ZIP: 19898
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: Macintosh System, 6.0
 SOFTWARE: Microsoft Word, 4.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/401,660
 FILING DATE: 10-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 200,373
 FILING DATE: 18-FEB-1994
 APPLICATION NUMBER: 993,156
 FILING DATE: 18-DEC-1992
 APPLICATION NUMBER: 236,967
 FILING DATE: 25-AUG-1988
 SEQ ID NO:1
 LENGTH: 49

RESULT 6
 US-116641-1
 ATTENTION NO. 5516641
 APPLICANT: OLLMAN, EDWIN F.; GOODMAN, THOMAS C.;
 TULLI, PAUL D.
 TITLE OF INVENTION: METHOD FOR DETECTION OF SPECIFIC
 NUCLEIC ACID SEQUENCES
 NUMBER OF SEQUENCES: 4
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/401,660
 FILING DATE: 10-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 200,373
 FILING DATE: 18-FEB-1994
 APPLICATION NUMBER: 993,156
 FILING DATE: 18-DEC-1992
 APPLICATION NUMBER: 236,967
 FILING DATE: 25-AUG-1988
 SEQ ID NO:1
 LENGTH: 49

RESULT 6
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 Query Match 0.4%; Score 16; DB 6; Length 49;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 US-09-364-543-84
 Sequence 84, Application US/09364543B
 Patent No. 6333394
 GENERAL INFORMATION:
 APPLICANT: Ruckman, Judy
 APPLICANT: Gold, Larry
 APPLICANT: Stephens, Andrew
 TITLE OF INVENTION: Nucleic Acid Ligands to Integrins
 FILE NUMBER: NE82
 CURRENT APPLICATION NUMBER: US/09/364-543B

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; CLONE: 86-H23
; FEATURE: /product= "protein"
; NAME/KEY: CDS
; LOCATION: 2..88
; OTHER INFORMATION: /function= "synthetic storage protein"
; OTHER INFORMATION: /product= "protein"
; OTHER INFORMATION: /gene= "ssp"
; OTHER INFORMATION: /standard_name= "5..8..5"
US-08-182-175A-48

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QY 2187 CTCCTCCATCTCTTC 2202
Db 52 CTCCTCCATCTCTTC 37

RESULT 10
US-08-823-771-57/C
; Sequence 57, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF PROTEINS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,633A
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGEL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: E. coli
; CELL TYPE: DH5 alpha
; IMMEDIATE SOURCE:
; CLONE: 86-H23
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..88
; OTHER INFORMATION: /function= "synthetic storage protein"
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; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; US-08-890-979-64

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Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2777 AGGCTGAGGAATGA 2791
Db 4 AGGCTGAGGAATGA 18

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RESULT 14

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; US-09-032-894-64
; Sequence 64, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-032-894-64

Query Match 0.4%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Query Match 0.4%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2777 AGGCTGAGGAATGA 2791
Db 4 AGGCTGAGGAATGA 18

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RESULT 15

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; US-09-031-626-64
; Sequence 64, Application US/09031626
; Patent No. 6228511
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
;
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; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; MEDIUM: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-031-626-64

Query Match 0.4%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2777 AGGCTGAGGAATGA 2791
Db 4 AGGCTGAGGAATGA 18

Search completed: January 11, 2003, 06:08:28
Job time : 121 secs

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GenCore version 5.1.3
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Om nucleic - nucleic search, using sw model

Run on: January 11, 2003, 01:49:57 ; Search time 4886 Seconds
 (without alignments)
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 Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

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 Maximum DB seq length: 100

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11: gb_htc:*

12: gb.est3:*

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19: em_gss_inv:*

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RESULTS

RESULT 1
 LOCUS AA833564/c
 DEFINITION AA833564 Soares-testis_NHT mRNA linear EST 31-DEC-1998
 mRNA sequence.
 ACCESSION AA833564
 VERSION AA833564.1 GI:2907292
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 96)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsr@mail.nih.gov
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
 , Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www-bi.llnl.gov/bbrp/image/image.html
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 High quality sequence stop: 55.

SUMMARIES

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c 3	21	0.6	74 14	D18644
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		/sex="male"
		/lab_host="DH10B"
		/note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TCTTACCACTCTGAACTGGGAGCGGCCATTTTTTTTTT 3'].
		Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization to Cots5, and was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	36 a	Best Local Similarity 100.0%; Pred. No. 5.6e-29; Length 96; Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN	14 c	Query Match 2.4%; Score 89; DB 9; Length 96; Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 2	AZ822704/c	Best Local Similarity 100.0%; Pred. No. 5.6e-29; Length 96; Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	3625 TGGCCCTGACTTGATGTTGTCAGAAATGCCAATCAATAAAGTGATATGCTT	91 bp DNA linear GSS 20-FEB-2001
Db	96 TGGCTCTGACTTGATGTTGTCAGAAATGCCAATCAATAAAGTGATATGCTT	364
VERSION	AZ822704.1	37
KEYWORDS	GSS.	
SOURCE	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 91)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenon,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid Inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu	
BASE COUNT	28 a	Best Local Similarity 100.0%; Pred. No. 4.2e-02; Length 91; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN	19 c	Query Match 0.6%; Score 23; DB 17; Length 91; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 3	D18644	0.6%; Score 23; DB 17; Length 91; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
BASE COUNT	20 a	Best Local Similarity 100.0%; Pred. No. 4.2e-02; Length 91; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN	20 g	Query Match 0.6%; Score 21; DB 14; Length 74; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FEATURES	source	Location/Qualifiers
		1. .74
		/organism="Mus musculus domesticus"
		/strain="C57BL/6J"
		/db_xref="taxon:10092"
		/clone="md0279"
		/clone_lib="Mouse 3'-directed"
		/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
BASE COUNT	20 a	Best Local Similarity 100.0%; Pred. No. 4.2e-02; Length 74; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN	17 g	Query Match 0.6%; Score 21; DB 14; Length 74; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
BASE COUNT	22 t	Best Local Similarity 100.0%; Pred. No. 4.2e-02; Length 74; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN	1 others	Query Match 0.6%; Score 21; DB 14; Length 74; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FEATURES	source	Location/Qualifiers
		1. .91
		/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="UGGC2M0096K08"

LOCUS	A2322055	75 bp	DNA	linear	GSS
DEFINITION	1M0042L19R Mouse 10kb plasmid UGGC1M library	Mus musculus	genomic		20-SEP-2000
CLONE	UGGC1M0042L19 R, DNA sequence.				
REFERENCE	A2322055				
AUTHORS	A2322055.1				
VERSION	GI:10375410				
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
MATERIALS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 75)				
Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenem,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedernhausen,A. and Wright,D., Weiss,R.					
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177				
FEATURES	High quality sequence stop: 75.				
source	Location/Qualifiers				
	1. 75				
	/organism="Mus musculus"				
	/strain="C57BL/6J"				
	/db_xref="taxon:10090"				
	/clone="UGGC1M0042L19"				
	/clone_id="Mouse 10kb plasmid UGGC1M library"				
	/sex="Male"				
	/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"				
	/note="Vector: FWD42Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory. Mouse DNA Resource				
	(http://www.jax.org/resources/documents/analyse/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA Polymerase and T4 Polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of FWD42 (9114732114gbAF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
BASE COUNT	46 a 15 g 5 t	9 c			
ORIGIN					

RESULT 7
A2322055/c

RESULT
A181069

LOCUS		DEFINITION		COMMENT	
AI80694	tujh00.x1	NCI_CGAP_Pr28	80 bp mRNA	linear EST	EST 07-JUL-1999
		Homo sapiens cDNA clone IMAGE:2251533			
		similar to contains element L1 repetitive element ; mRNA sequence.			
AI80694		NCI_CGAP			
AI810694.1					
		EST.			
		human.			
		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
		1 (bases 1 to 80)			
		NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
		Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.			
		CDNA Library Preparation: M. Bento Soares, Ph.D.			
		CDNA Library Arrayed by: Greg Lennon, Ph.D.			
		DNA Sequencing by: Washington University Genome Sequencing Center			
		Clone distribution: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.			
		www-bio.llnl.gov/bbp/image.html			
		Seq primer: -400P from Gibco			
		High quality sequence stop: 68.			
		Location/Qualifiers			
		1. .80			
		/organism="Homo sapiens"			
		/db_xref="IMAGE:2251553"			
		/clone_id="NCI_CGAP_Pr28"			
		/sex="male"			
		/dev_stage="adult"			
		/lab_host="DH10B"			
		/note="Organ: prostate; Vector: pT7 ³ D-Pac (Pharmacia)			
		with a modified polylinker; plasmid DNA from the			
		normalized library NCI_CGAP_Pr28 was prepared, and ss			
		circles were made in vitro. Following Hap purification,			
		this DNA was used as tracer in a subtractive hybridization			
		reaction. The driver was PCR-amplified cDNAs from a pool			
		of 5,000 clones made from the same library (cloneIDs			
		985608-986759, 1101192-1101959, and 1217928-1240615);			
		Subtraction by Bento Soares and M. Ratima Bonaldo."			
		ORIGIN			
RESULT 9	152721/c	Query Match	0.5%; Score 19; DB 9; Length 80;		
		Best Local Similarity	100.0%; Pred. No. 3.3e+03;		
		Matches	19; Conservative 0; Mismatches 0;		
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QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	15	TCTCTCTCTTCTTCTT	33		
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		3 a	2 g	68 t	
		7 c			
		ORIGIN			
RESULT 9	152721/c	Query Match	0.5%; Score 19; DB 14; Length 99;		
		Best Local Similarity	100.0%; Pred. No. 3.2e+03;		
		Matches	19; Conservative 0; Mismatches 0;		
		Indels	0; Gaps 0;		
QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
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		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
		Best Local Similarity	100.0%; Pred. No. 3.2e+03;		
		Matches	19; Conservative 0; Mismatches 0;		
		Indels	0; Gaps 0;		
QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
		BASE COUNT			
		41 a	14 c	16 g	
		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
		Best Local Similarity	100.0%; Pred. No. 3.2e+03;		
		Matches	19; Conservative 0; Mismatches 0;		
		Indels	0; Gaps 0;		
QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
		BASE COUNT			
		41 a	14 c	16 g	
		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
		Best Local Similarity	100.0%; Pred. No. 3.2e+03;		
		Matches	19; Conservative 0; Mismatches 0;		
		Indels	0; Gaps 0;		
QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
		BASE COUNT			
		41 a	14 c	16 g	
		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
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		Indels	0; Gaps 0;		
QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
		BASE COUNT			
		41 a	14 c	16 g	
		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
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		Matches	19; Conservative 0; Mismatches 0;		
		Indels	0; Gaps 0;		
QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
		BASE COUNT			
		41 a	14 c	16 g	
		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
		Best Local Similarity	100.0%; Pred. No. 3.2e+03;		
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QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
		BASE COUNT			
		41 a	14 c	16 g	
		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
		Best Local Similarity	100.0%; Pred. No. 3.2e+03;		
		Matches	19; Conservative 0; Mismatches 0;		
		Indels	0; Gaps 0;		
QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
		BASE COUNT			
		41 a	14 c	16 g	
		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
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		Matches	19; Conservative 0; Mismatches 0;		
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QY	2568	TCTCTCTCTTCTTCTT	2586		
Db	57	TCTCTCTCTTCTTCTT	39		
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Db	57	TCTCTCTCTTCTTCTT	39		
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		41 t	24 t	4 others	
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RESULT 10	AI207866	Query Match	0.5%; Score 19; DB 14; Length 99;		
		Best Local Similarity	100.0%; Pred. No. 3.2e+03;		
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		41 t	24 t	4 others	
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		BASE COUNT			
		41 a	14 c	16 g	
		41 t	24 t	4 others	
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		BASE COUNT			
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		Indels	0; Gaps 0;		
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Db	57	TCTCTCTCTTCTTCTT	39		
		BASE COUNT			
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		41 t	24 t	4 others	
		ORIGIN			
RESULT 10	AI207866	Query Match	0		

ORGANISM MUS musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 99)
 AUTHORS Melton,D., Brown,J., Kent,Y., Bresnick,A., Lee,C., Kaestner,K.,
 Lemishka,I., Seacrest,M., Permutt,A., Lee,C., Kaestner,K.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blustain,A.,
 Schmidt,A., Theising,B., Ritter,E., Ronco,I., Bennett,J., Cardenas,
 M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
 Jackson,Y. and Bowers,Y.
 TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Other_ESTs: 1109b02.y1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center This clone is
 available royalty-free through LBNL; Please contact the IMAGE
 consortium (info@image.lnl.gov) for further information
 Seq primer: -40bp from Gibco
 High quality sequence stop: 84.

FEATURES source
 Location/Qualifiers
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 (Life Technologies). cDNA made by oligo-dT priming.
 Size-selected by column fractionation; average insert size
 0.97 kb. Amplified once on solid support. cDNA Library
 Preparation: Guolin Chen."
 BASE COUNT
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 9e+03; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2961 ACTTACCAATGAAATT 2978
 Db 46 ACTTACCAATGAAATT 29

Search completed: January 11, 2003, 03:15:09
 Job time : 4892 secs

2 Seconds
 (nts)
 n cell updates/sec

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 Sequence 30, APP1
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 Sequence 951, APP1
 Sequence 952, APP1
 Sequence 953, APP1
 Sequence 3541, APP1
 Sequence 117, APP1
 Sequence 32, APP1
 Sequence 17, APP1
 Sequence 13, APP1
 Sequence 32, APP1
 Sequence 65, APP1
 Sequence 96, APP1
 Sequence 9, APP1
 Sequence 67, APP1
 Sequence 69, APP1
 Sequence 44, APP1
 Sequence 50, APP1
 Sequence 59, APP1
 Sequence 61, APP1
 Sequence 3879, APP1
 Sequence 3880, APP1
 Sequence 3881, APP1
 Sequence 3882, APP1
 Sequence 3883, APP1

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 38 0.4 100 10 US-09-865-108-970
 39 0.4 100 10 US-09-865-108-971
 40 0.4 100 10 US-09-865-108-972
 41 0.4 100 10 US-09-865-108-973
 42 0.4 100 10 US-09-865-108-974
 43 0.4 100 10 US-09-865-108-975
 44 0.4 100 10 US-09-865-108-976
 45 0.4 100 10 US-09-865-108-977

10 0.4 100 10 US-09-866-108-3882
 10 0.4 100 10 US-09-866-108-3883

ALIGMENTS

RESULT 1

US-09-810-796-7

; Sequence 7, Application US/09810796

; Patent No. US20020102677A1

; GENERAL INFORMATION:

; APPLICANT: Jegla, Timothy James

; APPLICANT: Icagen, Inc.

; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel

; FILE REFERENCE: 018512-005010US

; CURRENT APPLICATION NUMBER: US/09-810,796

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 60/190,954

; PRIOR FILING DATE: 2000-03-21

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:antisense

; OTHER INFORMATION: Primer (2)

US-09-810-796-7

Query Match 0.4%; Score 16; DB 10; Length 26;

Sequence 2705, AP Best Local Similarity 100.0%; Pred. No. 6e-02;

Sequence 2705, AP Matches 16; Conservative 0; Mismatches 0;

Sequence 84, AP Indels 0; Gaps 0;

Sequence 5, APPLICANT: Mcswiggen, James

Sequence 320, APPLICANT: Roberts, Beth

Sequence 71, APPLICANT: Pavco, Pamela

Sequence 1323, APPLICANT: Blatt, Lawrence

Sequence 1323, APPLICANT: Mcswiggen, James

Sequence 13, APPLICANT: Roberts, Beth

Sequence 1323, APPLICANT: Pavco, Pamela

RESULT 2

US-09-504-231A-2705/C

; Sequence 2705, Application US/09504231A

; Patent No. US200201458A1

; GENERAL INFORMATION:

; APPLICANT: Blatt, Lawrence

; APPLICANT: Mcswiggen, James

; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela

APPLICANT: Macejak, Dennis
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED TO HEPATITIS C VIRUS INFECTION

PRIOR APPLICATION: PPI 247/282

CURRENT APPLICATION NUMBER: US/09/504,231A

PRIOR FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: 09/257,608

PRIOR FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: 60/100,842

PRIOR FILING DATE: 1998-03-18

PRIOR APPLICATION NUMBER: 60/083,217

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3242

SOFTWARE: Patentin version 3.0

SEQ ID NO: 2705

LENGTH: 36

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Mole

US-09-504-231A-2705

Query Match Best Local Similarity 0.4%; Score 16; DB 10; Length 36; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 603 CCTCATCAGCTCTGAA 618

Db 16 CCTCATCAGCTCTGAA 1

RESULT 3
US-09-274-553D-2705/C

; Sequence 2705, Application US/09/274553D

GENERAL INFORMATION:

APPLICANT: Blatt, Lawrence

APPLICANT: McSwiggen, James

APPLICANT: Roberts, Beth

APPLICANT: Pavco, Pamela

APPLICANT: Morejek, Dennis

TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED TO HEPATITIS C VIRUS INFECTION

FILE REFERENCE: PPI 247/282

CURRENT APPLICATION NUMBER: US/09/274,553D

CURRENT FILING DATE: 1999-03-23

PRIOR APPLICATION NUMBER: 09/257,608

PRIOR FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: 60/100,842

PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/083,217

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 3148

SOFTWARE: Patentin version 3.0

SEQ ID NO: 2705

LENGTH: 36

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Mole

US-09-274-553D-2705

Query Match Best Local Similarity 0.4%; Score 16; DB 10; Length 36; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 603 CCTCATCAGCTCTGAA 618

Db 16 CCTCATCAGCTCTGAA 1

RESULT 4
US-10-024-997-84

; Sequence 84, Application US/10024997

PATENT NO. US2003015036A1

GENERAL INFORMATION:

APPLICANT: Ruckman, Judy

APPLICANT: Gold, Larry

APPLICANT: Stephens, Andrew

APPLICANT: Jainji, Nebojsa

TITLE OF INVENTION: Nucleic Acid Ligands to Integrins

FILE REFERENCE: NEX82

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 09/364,543

PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 84

LENGTH: 87

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

NAME/KEY: modified_base

LOCATION: (1),(87)

OTHER INFORMATION: All pyrimidines are 2' F.

US-10-024-997-84

Query Match Best Local Similarity 75.0%; Score 16; DB 12; Length 87; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3350 ATCCACACCTGGCTTG 3365

Db 23 AUCCACACCCUGCGUUG 38

RESULT 5
US-09-859-214-5

; Sequence 5, Application US/09859214

PATENT NO. US2002010311A1

GENERAL INFORMATION:

APPLICANT: Schwerder, Charles F.

APPLICANT: Shroff, Hitesh N.

TITLE OF INVENTION: INHIBITORS OF MACAM-1-MEDIATED

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02421

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/859,214

FILING DATE: 16-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/109,879

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/582,740

FILING DATE: 04-Jan-1996

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: LRS95-12A2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 861-6240
 TELEFAX: (781) 861-9540
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 36 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-859-214-5

RESULT 6
 Query Match 0.4%; Score 15; DB 10; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Mismatches
 Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 1449 CCTGGATCCATCC 1463
 Db 11 CCATGGAATCCATCC 25

RESULT 6
 Query Match 0.4%; Score 15; DB 10; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Mismatches
 Matches 15; Conservative 0; Indels 0; Gaps 0;

US-09-205-658-320/C

; Sequence 320, Application US/09205658

GENERAL INFORMATION:

APPLICANT: Ruvkin, Gary

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

FILE REFERENCE: 00786/351004
 CURRENT APPLICATION NUMBER: US/09/205, 658

EARLIER APPLICATION NUMBER: 08-857, 076

EARLIER FILING DATE: 1997-05-15

EARLIER APPLICATION NUMBER: 08-888, 534

EARLIER FILING DATE: 1997-07-07

EARLIER APPLICATION NUMBER: US/88/10080

EARLIER FILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 328

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 320

LENGTH: 44

TYPE: DNA

ORGANISM: Caenorhabditis elegans

US-09-205-658-320

Query Match 0.4%; Score 15; DB 10; Length 44;

Best Local Similarity 100.0%; Pred. No. 2e+03; 0; Mismatches
 Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 339 CGAGAGAGGAAGA 353
 Db 36 CGAGAGAGAGAGAGA 22

RESULT 7
 US-09-756-095-71

; Sequence 71, Application US/09756095

PATENT NO. US20020115207A1

GENERAL INFORMATION:

APPLICANT: Mitchell, Lloyd G.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN

FILE REFERENCE: A31304-B4 072874.0134

CURRENT APPLICATION NUMBER: US/09/756, 095

CURRENT FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: 09/158, 863

PRIOR FILING DATE: 1998-09-23

PRIOR APPLICATION NUMBER: 09/133, 717

PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: 09/087, 233

PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 08/766, 354
 PRIOR FILING DATE: 1996-12-13
 PRIOR APPLICATION NUMBER: 60/008, 317
 PRIOR FILING DATE: 1995-12-07
 NUMBER OF SEQ ID NOS: 105
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 71
 LENGTH: 47
 TYPE: DNA
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Branch point, pyrimidine tract and acceptor splice
 OTHER INFORMATION: site of PTM

RESULT 8
 US-09-946-807-1323
 Sequence 1323, Application US/09946807
 GENERAL INFORMATION:

APPLICANT: Stefansson, Hreinn

APPLICANT: Steinthorsdottir, Valgerdur

TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE

FILE REFERENCE: 2345.2004-001

CURRENT APPLICATION NUMBER: US/09/946, 807

PRIOR APPLICATION NUMBER: US/09/795, 668

PRIOR FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US 09/515, 716

PRIOR FILING DATE: 2000-02-28

NUMBER OF SEQ ID NOS: 1531

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1323

LENGTH: 61

TYPE: DNA

ORGANISM: Homo sapiens

US-09-946-807-1323

Query Match 0.4%; Score 15; DB 9; Length 61;

Best Local Similarity 100.0%; Pred. No. 2.1e+03; 0; Mismatches
 Matches 15; Conservative 0; Indels 0; Gaps 0;

Qy 3628 CCTCTACTTGTATT 3642
 Db 12 CCTCTACTTGTATT 26

RESULT 9
 US-09-795-668-1323
 Sequence 1323, Application US/09795668
 GENERAL INFORMATION:

APPLICANT: Stefansson, Hreinn

APPLICANT: Steinthorsdottir, Valgerdur

APPLICANT: Gulcher, Jeffrey R.

TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE

FILE REFERENCE: 2345.2004-001

CURRENT APPLICATION NUMBER: US/09/795, 668

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US 09/515, 716

PRIOR FILING DATE: 2000-02-28

NUMBER OF SEQ ID NOS: 1531

SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1323
 LENGTH: 61
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-795-686-1323

Query Match 0.4%; Score 15; DB 10; Length 61;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3628 CCTCTACTTGTATT 3642
 Db 12 CCTCTACTTGTATT 26

RESULT 10
 US-09-795-686-1323
 Sequence 1323, Application US/09795686
 Patent No. US2002094954A1
 GENERAL INFORMATION:
 APPLICANT: Stefansson, Hreinn
 APPLICANT: Steinthorsdottir, Valgerdur
 APPLICANT: Gulcher, Jeffrey R.
 TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
 FILE REFERENCE: 2345, 2005-001
 CURRENT APPLICATION NUMBER: US/09/795, 686
 PRIOR FILING DATE: 2001-02-28
 PRIOR FILING DATE: 2000-02-28
 NUMBER OF SEQ ID NOS: 1331
 SEQ ID NO 1323
 LENGTH: 61
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-795-686-1323

Query Match 0.4%; Score 15; DB 10; Length 61;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3628 CCTCTACTTGTATT 3642
 Db 12 CCTCTACTTGTATT 26

RESULT 11
 US-10-076-248-13
 Sequence 13, Application US/10076248
 Publication No. US20020193580A1
 GENERAL INFORMATION:
 APPLICANT: Mitchell, Lloyd
 APPLICANT: Garcia-Blanco, Mariano
 APPLICANT: Puttaraju, Madhavi
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
 TITLE OF INVENTION: SPliceosome Mediated RNA Trans-Splicing
 CURRENT FILING DATE: US/10/07/6,248
 CURRENT FILING DATE: A31304B-A-F 039906-0105
 CURRENT FILING DATE: 2002-02-12
 PRIOR APPLICATION NUMBER: 09/411,492
 PRIOR FILING DATE: 2001-08-29
 PRIOR APPLICATION NUMBER: 09/438,858
 PRIOR FILING DATE: 2001-04-20
 PRIOR APPLICATION NUMBER: 09/556,096
 PRIOR FILING DATE: 2001-01-08
 PRIOR APPLICATION NUMBER: 09/5158,863
 PRIOR FILING DATE: 1998-03-23
 PRIOR APPLICATION NUMBER: 09/133,717
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: 09/087,233
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 08/766,354

Query Match 0.4%; Score 15; DB 10; Length 61;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3628 CCTCTACTTGTATT 3642
 Db 12 CCTCTACTTGTATT 26

RESULT 12
 US-09-020-300A-1268/c
 Sequence 1268, Application US/09920300A
 Patent No. US20020136728A1
 GENERAL INFORMATION:
 APPLICANT: King, Gordon E.
 APPLICANT: Meagher, Madeline Joy
 APPLICANT: Xu, Jiangchun
 APPLICANT: Sociist, Heather
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
 FILE REFERENCE: 210121-547
 CURRENT APPLICATION NUMBER: US/09/920,300A
 CURRENT FILING DATE: 2001-07-31
 NUMBER OF SEQ ID NOS: 1789
 SEQ ID NO 1268
 LENGTH: 73
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE: NAME/KEY: misc_feature
 LOCATION: 53
 OTHER INFORMATION: n = A,T,C or G
 US-09-920-300A-1268

Query Match 0.4%; Score 15; DB 10; Length 73;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2602 ACCACACGACACA 2616
 Db 68 AGCACACGACACA 54

RESULT 13
 US-10-033-528-1268/c
 Sequence 1268, Application US/10033528
 Patent No. US20020131971A1
 GENERAL INFORMATION:
 APPLICANT: King, Gordon E.
 APPLICANT: Meagher, Madeline Joy
 APPLICANT: Xu, Jiangchun
 APPLICANT: Sociist, Heather
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
 FILE REFERENCE: 210121-547C1
 CURRENT APPLICATION NUMBER: US/10/033,528
 CURRENT FILING DATE: 2001-12-26
 NUMBER OF SEQ ID NOS: 1896

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 1268
LENGTH: 73
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: 53
OTHER INFORMATION: n = A,T,C or G
US-10-033-528-1268

Query Match 0.4%; Score 15; DB 12; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2602 AGCACACAGCACCA 2616
Db 68 AGCAQACAGCACCA 54

RESULT 14
US-09-864-761-31308/c
Sequence 31308, Application US/09864761
; Patent No. US2002004863A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SEQ ID NO 31308

Query Match 0.4%; Score 15; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2568 TTCTCTCTCTTTT 2582
Db 17 TTCTCTCTTTT 3

RESULT 15
US-09-878-574-6583
Sequence 6583, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(154)01.B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 6583
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701098625H1
US-09-878-574-6583

Query Match 0.4%; Score 15; DB 10; Length 76;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2198 TCTTCCTGAGAGA 2212
Db 53 TCTTCCTGAGAGA 67

Search completed: January 11, 2003, 06:06:14
Job time : 154 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model.

Run on: January 11, 2003, 01:51:27 ; Search time 717 Seconds
(without alignments)

11662.022 Million cell updates/sec

Title: US-10-003-354-3

Perfect score: 3713

Sequence: attaacaggcgtgtttagg.....aaacttaatgagtattta 3713

Scoring table: Oligo_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002:*

1: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1980.DAT:*

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15: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1997.DAT:*

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21: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

ID ABN41013
ID ABN41013 standard; DNA; 60 BP.

XX ABN41013;

XX ABN41013;

DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:13761.

XX KW Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX PN WO200210449-A2.

PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-1B01903.

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX PA (COMP-) COMPUGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI: 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	60	1.6	60 24 ABN41013	Human spliced tran
2	19	0.5	50 23 ABL01023	Human SNP involvin
c 3	18	0.5	36 13 AAQ23486	Purine rich HUMINT
c 4	18	0.5	51 22 AAH40868	Human SNP flanking
5	18	0.5	60 24 ABM41363	Human spliced tran
6	17	0.5	25 21 AAC98031	HLA HLA-C gene PCR
c 7	17	0.5	33 22 AAH41655	Hexokinase protein
9	17	0.5	38 17 AAT40778	Primer for HPV6a L
17	0.5	41 22 AAH46168	Hexokinase protein	
				Feline parvoviral
				Human SNP flanking
				Human stemolysin
				Human gene signature
				Human gene signature
				Human map-related
				Human SNP oligonuc
				Human silent SNP c
				Staphylococcus aur
				Human secreted pro
				Human biallelic Po
				Human spliced tran
				Human spliced tran
				Human silent SNP c
				Staphylococcus aur
				Human secreted pro
				Human spliced tran
				Human spliced tran
				Human NS3 protease 1
				Generic HCV NS3 pr
				Human NS3 protease 1
				Rat spliced trans
				C. utilis crti pri
				HCV NS3 protease 1
				HGF nucleic acid 1
				Integrin alpha V b
				Antisense strand n
				Clone 86H23 used
				SSP 5.8.3.5 clone
				Synthetic storage
				Synthetic Lysine-r
				Hammerhead ribozym

PT a genome, useful for detecting tissue-, pathology- and
 PT developmental-specific genes
 XX
 PS Example 1; SEQ ID 13761; 47pp; English.
 XX
 The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcripts. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59569 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.
 N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.

SQ Sequence 60 BP; 23 A; 15 C; 15 G; 7 T; 0 other;

Query Match 1.6%; Score 60; DB 24; Length 60;
 Best Local Similarity 100.0%; Pred. No. 3.4e-10; Mismatches 0; Indels 0; Gaps 0;

QY 1130 AAAATGACCTCAAGGCTCAACCTACAAACGCGGGTTCCAGAAGAGGGAGAG 1189
 Db 1 AAAATGACCTCAAGGCTCAACCTACAAACGCGGGTTCCAGAAGAGGGAGAG 60

RESULT 2

ABL01023
 ID ABL01023 standard; DNA; 50 BP.
 AC
 XX
 DT 05-MAR-2002 (first entry)

DE Human SNP involving a gap oligonucleotide SEQ ID NO:1014.
 XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic; KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease; KW infection; polymorphic protein; ds.
 KW Homo sapiens.
 XX WO200138586-A2.

XX 31-MAY-2001.
 XX 22-NOV-2000; 2000WO-US32311.
 PR 24-NOV-1999; 99US-0167383.
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 PT Shinkets RA, Leach M;
 DR WPI; 2001-355949/37.

XX Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence polymorphism -
 XX
 PS Claim 1; Page 554; 674pp; English.
 XX
 ABL0010 to ABL01104 represent human nucleic acid oligonucleotides comprising one or more single nucleotide polymorphisms (SNPs). ABB56531 to ABB6903 represent human peptides encoded by some of the SNP oligonucleotides. The sequences from the present invention can have immunosuppressive, cytostatic, antiinflammatory, neuroprotective and antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides and antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism. The pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterized polymorphism are present in individuals. The antibodies may be used in the detection, quantification and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein within appropriate physiological samples).

SQ Sequence 50 BP; 1 A; 11 C; 2 G; 36 T; 0 other;

Query Match 0.5%; Score 19; DB 23; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2567 TTCTCTCTCTTTTTT 2585
 Db 8 TTCTCTCTCTTTTTT 26

RESULT 3

AAQ25486/C
 ID AAQ25486 standard; DNA; 36 BP.
 XX
 AC AAQ25486;
 DT 07-DEC-1992 (first entry)

XX DE Purine rich HUMINR02 target duplex sequence.
 XX Target; human leukocyte adhesion protein p150.95 alpha subunit gene; AIDS; triplex; HIV; hepatitis; malignancy; inflammation; ds.
 KW
 XX OS Synthetic.
 XX
 PN WO9209705-A.
 XX
 PD 11-JUN-1992.
 XX
 PF 25-NOV-1991; 91WO-US08811.

XX
 PR 23-NOV-1990; 90US-0517907.
 PR 18-JAN-1991; 91US-0643382.
 PR 08-APR-1991; 91US-0683420.
 PR 17-APR-1991; 91US-0886544.
 PR 17-APR-1991; 91US-0886545.
 PR 17-APR-1991; 91US-0886547.
 PR 27-SEP-1991; 91US-0766733.
 XX
 PA (GILE-) GILEAD SCI INC.
 XX
 PT Froehler B, Krawczyk S, Matteucci MD, Milligan J;
 XX
 PT WPI; 1992-217083/26.

XX New Oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes, malignancy and inflammation

XX

PS Claim 11; Page 64; 77pp; English.

XX

CC The sequence depicts a HOMINT02 sequence beginning at nucleotide 2370. The sequence is a viral duplex sequence which contains a purine-rich region concentrated on one chain of the duplex. The sequence may be prep. by standard DNA synthesis.

CC The duplex sequence is used as a target for novel oligomers which are capable of forming a triplex at physiological pH by coupling into the major groove of the DNA duplex. Two such oligomers LAP 321-2 are capable of forming a triplex with this sequence. The oligomers are used in the treatment of inflammation. Similar oligomers may be used to target viral DNA duplexes specific for HIV, herpes and other viruses. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also A025452-25501 and A030226-448.

SQ Sequence 36 BP; 27 A; 0 C; 9 G; 0 U; 0 other;

Query Match 0.5%; Score 18; DB 13; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.4e-02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2568 TTCTCTCTCTTTTTT 2585

Db 18 TTCTCTCTCTTTTTT 1

RESULT 4

AAH40868

ID AAH40868 standard; DNA; 51 BP.

AC

XX AAH40868;

DT 14-AUG-2001 (first entry)

XX Human SNP flanking oligonucleotide SEQ ID 3664.

DE

XX single nucleotide polymorphism; SNP; single nucleotide primer extension; SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; ds.

KW

XX

OS Homo sapiens.

XX

PN WO200129262-A2.

XX

PD 26-APR-2001.

XX

PR 13-OCT-2000; 2000WO-US28436.

XX

PR 15-OCT-1999; 99US-0160096.

XX

PA (ORCH-) ORCHID BIOSCIENCES INC.

XX

PI Picoult-Newburg L, Pohl M;

XX

DR WPI; 2001-290930/30.

PS Claim 1; Page 68; 83pp; English.

XX

CC sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a

CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.

CC The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial diseases of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a fragment of human DNA flanking the site of a single nucleotide polymorphism.

SQ Sequence 51 BP; 5 A; 15 C; 8 G; 23 T; 0 other;

Query Match 0.5%; Score 18; DB 22; Length 51;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2567 TTCTCTCTCTTTTTT 2584

Db 34 TTCTCTCTCTTTTTT 51

RESULT 5

ABN4133

ID ABN4133 standard; DNA; 60 BP.

AC

XX ABN4133;

XX

DT 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:14111.

XX Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

KW

XX Homo sapiens.

OS

PN WO200210449-A2.

XX

PD 07-FEB-2002.

XX

PF 20-JUL-2001; 2001WO-1R01903.

XX

PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX

PA (COMP-) COMPUTEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX

DR WPI; 2002-257383/30.

PS Example 1; SEQ ID 14111; 47pp; English.

XX

PT New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes

PT

XX

PT The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the transcriptome comprises messenger RNAs transcribed from multiple (sub-)transcriptome units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of

the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini-libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pdb/published_pct.html](http://wipo.int/pdb/published_pct.html).

Sequence 60 BP; 11 A; 21 C; 15 G; 13 T; 0 other; SQ

Query Match 0.5%; Score 18; DB 24; Length 60; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; AC

Qy 2727 TGCAGAGCAGCCTCTC 2744 Db 18 TGCCAGAACGAGCTCTC 35

RESULT 6 AAC96031

XX AAC96031 standard; DNA; 25 BP.

XX AAC96031; AC

XX DT 26-FEB-2001 (first entry)

XX HLA HLA-C gene PCR primer #43.

XX DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA; human leukocyte antigen; PCR primer; ss. KW

XX OS Homo sapiens.

XX WO20065088-A2.

XX PD 02-NOV-2000.

XX PP 20-APR-2000; 2000WO-EP03636.

XX PR 26-APR-1999; 99EP-0303215.

XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

XX PI Ulfendahl P, Wong K;

XX DR WPI: 2000-679577/66.

XX PS

XX Example 5; Page 17; 35pp; Chinese.

XX The invention relates to hexokinase protein 12 (AAB73785), nucleic acids encoding it (AAH46162), and a method for the recombinant production of hexokinase protein 12. The present invention additionally discloses an antagonist of hexokinase protein 12 for therapeutic use, and an antibody which specifically binds to hexokinase protein 12. Hexokinase protein 12, and nucleotides which encode it may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reactions or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences AAH46165-AAH46166 represent PCR primers used in 12 cDNA for cloning.

XX CC particular.

CC Sequence 25 BP; 1 A; 5 C; 2 G; 17 T; 0 other; SQ

Query Match 0.5%; Score 17; DB 22; Length 33; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; AC

Qy 2999 TTTTTTGTCTCTCTC 3015 Db 6 TTTTTTGTCTCTC 22

RESULT 7 AAH46165

XX DE AAH46165 standard; DNA; 33 BP.

XX AC AAH46165;

XX DT 21-SEP-2001 (first entry)

XX Hexokinase protein 12 PCR primer, SEQ ID NO:5.

XX KW Hexokinase protein 12; human; recombinant; production; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; inflammatory condition; cytostatic; anti-HIV; antiinflammatory; immunomodulator; PCR primer; ss. KW

XX OS Homo sapiens.

XX PN WO200147968-A1.

XX PD 05-JUL-2001.

XX PP 18-DEC-2000; 2000WO-CN00597.

XX PR 23-DEC-1999; 99CN-0125723.

XX PA (UYUU) UNIV FUDAN.

XX PA (SHAN) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.

XX PI Mao Y, Xie Y;

XX DR WPI: 2001-41827/44.

XX PT Hexokinase protein 12 and encoded polynucleotide, applicable in diagnosis and treatment of cancer, hemopathy, HIV infection, immunological diseases and phlogosis

XX PT Example 5; Page 17; 35pp; Chinese.

XX The invention relates to hexokinase protein 12 (AAB73785), nucleic acids encoding it (AAH46162), and a method for the recombinant production of hexokinase protein 12. The present invention additionally discloses an antagonist of hexokinase protein 12 for therapeutic use, and an antibody which specifically binds to hexokinase protein 12. Hexokinase protein 12, and nucleotides which encode it may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of its activity or for peptide fingerprinting identification. The polynucleotide can be used as a primer for nucleic acid amplification reactions or as a probe for hybridisation reactions, or in producing gene chips or microarrays. Sequences AAH46165-AAH46166 represent PCR primers used in 12 cDNA for cloning.

XX CC Sequence 33 BP; 9 A; 6 C; 9 G; 9 T; 0 other; SQ

Query Match 0.5%; Score 17; DB 22; Length 33; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; AC

QY 2692 CATGGTGTATGAGA 2708
 |||||||
 XX OS Homo sapiens.
 Db XX
 16 CATGGTGTATGAGA 32 PN WO200147968-A1.
 XX
 RESULT 8
 AAT40778/C XX
 ID AAT40778 standard; cDNA; 38 BP.
 XX
 AC AAT40778; XX
 XX DT 26-NOV-1996 (first entry) XX
 DE Primer for HPV6a L2 gene amplification.
 XX
 KW MNN9; Yeast; disrupt; human papilloma virus; capsid protein; prevent; vaccine; infection; treat; primer; PCR; probe; ss.
 XX OS Synthetic.
 XX PT (UYFU-) UNIV FUDAN.
 PN PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
 XX PD 05-JUL-2001.
 XX PF 18-DEC-2000; 2000WO-CN00597.
 XX DR 23-DEC-1999; 99CN-0125723.
 XX PT
 XX PA
 XX WO9615247-A1. XX
 XX
 PD 23-MAY-1996. XX
 XX PF 13-NOV-1995; 95WO-US15027.
 XX CC
 PR 14-NOV-1994; 94US-0339368. CC
 XX PA (MERI) MERCK & CO INC. CC
 XX PT
 PI Cook JC, George HA, Hofmann KJ, Jansen KU, Joyce JG; CC
 Lehman ED, Markusz, Schultz LD; XX
 DR WPI: 1995-268219/27. CC
 XX
 Papilloma virus capsid proteins, pref. L1, L2, L1 + L2 and derivs. - CC
 useful in vaccines to treat or prevent papillomavirus infection. CC
 XX
 PS Example 14; Page 30; 92pp; English. CC
 XX
 CC AAT40774-78 are primers used in the cloning of human papilloma virus (HPV) strain 6a capsid protein genes L1, L2 and L1+L2. Yeast strains contg. disrupted genes (see AAT40768-73) were used for the isolation of HPV capsid proteins. The capsid proteins are useful in vaccines to treat or prevent HPV infection. The present sequence is a 3' antisense primer used to amplify the HPV6a L2 gene. CC
 XX
 SQ Sequence 38 BP; 12 A; 12 C; 9 G; 5 T; 0 other; CC
 XX
 Query Match 0.5%; Score 17; DB 17; Length 38; CC
 Best Local Similarity 100.0%; Pred. No. 1.1e+03; CC
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CC
 QY 70 TTTTTTCAGATGIGC 86 CC
 |||||||
 Db 33 TTTTTTCAGATGIGC 17 CC
 XX
 RESULT 9
 AAH46167 XX
 ID AAH46167 standard; DNA; 41 BP.
 XX
 AC AAH46167; XX
 XX DT 21-SEP-2001 (first entry) XX
 DE Hexokinase protein 12 probe, SEQ ID NO:9.
 XX
 KW Hexokinase protein 12; human; recombinant production; XX
 KW malignant tumour; cancer; blood disease; HIV infection; XX
 KW human immunodeficiency virus; immune disorder; inflammatory condition; XX
 KW cytostatic; anti-HIV; antinflammatory; immunomodulator; probe; ss.
 XX OS Homo sapiens.
 XX PN WO200147968-A1.
 XX
 DE 05-JUL-2001.
 XX PF 18-DEC-2000; 2000WO-CN00597.
 XX PR 23-DEC-1999; 99CN-0125723.

XX (UYFU-) UNIV FUDAN.
 PA (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD.
 XX
 PT Mao Y, Xie Y;
 DR WPI: 2001-416227/44.
 XX
 PT Hexokinase protein 12 and encoded polynucleotide, applicable in
 diagnosis and treatment of cancer, hemopathy, HIV infection,
 immunological diseases and phlogosis -
 XX
 PS Example 7; Page 20; 35pp; Chinese.
 XX
 The invention relates to hexokinase protein 12 (AAB73785), nucleic acids
 encoding it (AAH46162), and a method for the recombinant production of
 hexokinase protein 12. The present invention additionally discloses an
 antagonist of hexokinase protein 12 for therapeutic use, and an antibody
 which specifically binds to hexokinase protein 12. Hexokinase protein 12,
 and nucleotides which encode it may be used for treating a variety of
 diseases such as malignant tumours, blood disease, HIV (human
 immunodeficiency virus) infection, immune disorders and inflammatory
 conditions. The protein may also be used to screen for modulators of its
 activity or for peptide fingerprinting identification. The polynucleotide
 can be used as a primer for nucleic acid amplification reactions or as a
 probe for hybridisation reactions, or in producing gene chips or
 microarrays. Sequences AAH4167-AAH46168 represent hexokinase protein 12
 probes used in an exemplification of the invention.
 XX
 Sequence 41 BP; 7 A; 6 C; 12 G; 16 T; 0 other;
 CC Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 2692 CATTGGTGTTATGAGA 2708
 DB 6 CATTGGTGTTATGAGA 22
 XX
 RESULT 11
 AAH8875/C
 AC AAT8875;
 XX
 DT 24-APR-1998 (first entry)
 DE Feline parvoviral VP1 T cell epitope encoding DNA.
 XX parvovirus; feline; canine; T cell epitope; VP1; VP2; vaccine;
 KW immunogen; nucleocapsid protein; cat; dog; mink; ss.
 XX
 OS Synthetic.
 OS Parvovirus.
 XX
 FH Key
 FT Location/qualifiers
 FT 7.48
 FT /*tag= a
 FT /note= "the stop codon is not indicated"
 XX
 PN WO9740163-A1.
 XX PD 30-OCT-1997.
 XX PF 18-APR-1997; 97WO-EP01943.
 PR 19-APR-1996; 96EP-0106217.
 XX PA (COLP-) COLPAN M.
 XX PI Baker HJ, Colpan M, Schorr J, Smith BF;
 XX
 DR WPI: 1997-535847/49.
 DR P-PSDB; ARW31733.
 XX
 PT Vaccine containing nucleic acid expressing parvoviral epitope -
 PT particularly both B and T cell epitope(s), for immunisation of cats,
 PT dogs and mink against Parvoviruses, also as a carrier for other
 PT antigens
 XX
 PS Claim 12; Page 15; 30pp; English.
 XX
 CC This synthetic nucleotide sequence encodes the T-cell epitope of a
 CC parvoviral VP1 nucleocapsid protein. This is used in the preparation of
 CC an anti-parvovirus vaccine. The anti-parvovirus vaccine contains nucleic
 CC acid encoding at least one parvovirus specific VP1 or VP2 T/B cell
 CC antigenic epitope plus a carrier. The anti-parvovirus vaccine are
 CC especially used to protect cats, dogs and mink, e.g. against feline
 CC panleukopenia virus, mink enteritis virus or gastroenteritis caused by
 CC canine parvovirus (CPV). The vaccine also includes an adjuvant,
 CC particularly a DNA containing unmethylated CGG motifs i.e. ISO. The ISO
 CC contains phosphorothioate linkages and is a powerful immune activator.
 CC The vaccine may also be used to deliver other immunogens e.g. (human)
 hepatitis B surface antigen. Immunisation with naked DNA provides good
 CC protection against parvovirus after only one injection. Both humoral and
 CC cellular responses may be induced.
 XX
 Sequence 48 BP; 19 A; 11 C; 9 G; 9 T; 0 other;
 CC Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 CC Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 2562 CCAGCTTCTCTCTCT 2578
 DB 47 CCAGCTTCTCTCT 31
 XX
 RESULT 12
 ANI39316/C
 ID AAH39316 standard; DNA; 51 BP.
 XX
 AC AAH39316;
 XX
 DT 14-AUG-2001 (first entry)
 DE Human SNP flanking oligonucleotide SEQ ID 2112.
 XX
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNP; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200129262-A2.
 XX
 PR 26-APR-2001.
 XX
 PR 13-OCT-2000; 2000WO-US28436.
 XX
 PR 15-OCT-1999; 99US-0160096.
 XX
 PR (ORCH-) ORCHID BIOSCIENCES INC.
 PR
 PR Picoult-Newburg L, Pohl M;
 XX
 DR WPI; 2001-290930/30.
 XX
 PR New genotyping oligonucleotide, useful for detecting the presence,
 PR absence or identity of single polynucleotide polymorphism in a nucleic
 PR acid sample -
 XX

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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39: em_htgo_hum: *
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HUMSPALTC/C
LOCUS HUMSPALTC
DEFINITION Homo sapiens nuclear autoantigen mRNA, partial cds; alternatively spliced.
ACCESSION L79986
VERSION L79986.1
KEYWORDS GI:18653899
SP100; alternative splicing; interferon-inducible protein; nuclear autoantigen.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherini; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 83)
AUTHORS Szostecki,C., Guldner,H.H., Netter,H.J. and Willi,H.

Pred. No. is the number of results predicted by chance to have a

A93509/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	A93509 Sequence 2 from Patent WO9740163. A93509 A93509.1 GI:6741728 unidentified. unclassified.	42 bp DNA linear PAT 22-JAN-2000		TITLE NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS JOURNAL Patent: WO 97/40163-A 7 JUN-1997; COLPAN METIN (DE); SCHORR JORCHIM (DE) Location/Qualifiers 1. .48 /organism="unidentified"
REFERENCE AUTHORS TITLE JOURNAL FEATURES source	1 (bases 1 to 42) Colpan,M. and Schorr,J. NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS PATENT: WO 97/40163-A 2 30-OCT-1997; COLPAN METIN (DE); SCHORR JORCHIM (DE) Location/Qualifiers 1. .42 /organism="unidentified" /db_xref="taxon:32644"	BASE COUNT 17 a ORIGIN 9 c 9 g 7 t		BASE COUNT 8 a ORIGIN 10 c 12 g 18 t
RESULT 6 A93513/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	A93513 Sequence 6 from Patent WO9740163. A93513 A93513.1 GI:6741732 unidentified. unclassified.	48 bp DNA linear PAT 22-JAN-2000		RESULT 8 AX116989/c LOCUS AX116989 DEFINITION Sequence 2112 from Patent WO0129262. ACCESSION AX116989 VERSION AX116989.1 KEYWORDS human. SOURCE Homo sapiens ORGANISM Mammalia; Eutetrapoda; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominoidea; Homo. REFERENCE 1 (bases 1 to 51) AUTHORS Picolli-Newburg,L. and Pohl,M. TITLE Genotyping reagents, kits and methods of use thereof JOURNAL Patent: WO 0129262-A 2112 26 APR-2001; Orchid Biosciences, Inc. (US) FEATURES Location/Qualifiers source 1. .51 /organism="Homo sapiens" /db_xref="taxon:9606"
REFERENCE AUTHORS TITLE JOURNAL FEATURES source	NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS PATENT: WO 97/40163-A 6 30-OCT-1997; COLPAN METIN (DE); SCHORR JORCHIM (DE) Location/Qualifiers 1. .48 /organism="unidentified"	BASE COUNT 19 a ORIGIN 11 c 9 g 9 t		BASE COUNT 20 a ORIGIN 9 c 7 g 15 t
RESULT 7 A93514 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	A93514 Sequence 7 from Patent WO9740163. A93514 A93514.1 GI:6741733 unidentified. unclassified. unclassified.	48 bp DNA linear PAT 22-JAN-2000		RESULT 9 I38031 LOCUS I38031 DEFINITION Sequence 1044 from patent US 5612215. ACCESSION I38031 VERSION I38031.1 KEYWORDS SOURCE Unknown. ORGANISM Unclassified. REFERENCE 1 (bases 1 to 54) AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T. TITLE Stromelysin targeted ribozymes JOURNAL Patent: US 5612215-A 1044 18 MAR-1997; FEATURES Location/Qualifiers source 1. .54 /organism="unknown" /db_xref="taxon:32644"
REFERENCE AUTHORS	1 (bases 1 to 48) Colpan,M. and Schorr,J.	BASE COUNT 18 a ORIGIN 9 c 18 g 9 t		Query Match 0.5%; Score 17; DB 6; Length 54;

Qy	3286	TCTGGGGAGAGAGGGG	3302	Best Local Similarity 100.0%; Pred. No. 2.5e+03; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Indels 0; Gaps 0;
Db	1	TCTGGGGAGAGAGGGG	17		
RESULT 10					
REFERENCE					
AUTHORS					
LOCUS	194881	194881	54 bp	DNA	linear
DEFINITION		Sequence 1044 from patent US 5731295.			PAT 01-DEC-1998
ACCESSION	194881				
VERSION	194881.1	GT:3939351			
KEYWORDS					
SOURCE		Unknown.			
ORGANISM		Unclassified.			
FEATURES		1. (bases 1 to 54)			
source		Draper, K.G., Pavco, P., McSwiggen, J., Gustafson, J. and			
BASE COUNT	18 a	18 a	9 c	18 g	9 t
ORIGIN					
Query Match		0.5%; Score 17; DB 6; Length 54;			
Best Local Similarity		100.0%; Pred. No. 2.5e+03;			
Matches		17; Conservative 0; Mismatches 0;			
Indels		0; Gaps 0;			
Qy	3286	TCTGGGGAGAGAGGGG	3302	Method of reducing stromelysin RNA via ribozymes	
Db	1	TCTGGGGAGAGAGGGG	17	Patent: US 5731295-A 104 24-MAR-1998; Location/Qualifiers	
RESULT 11					
REFERENCE					
AUTHORS					
LOCUS	AX422998	AX422998	65 bp	DNA	linear
DEFINITION		Sequence 298 from Patent WO2002053728.			PAT 16-AUG-2002
ACCESSION	AX422998				
VERSION	AX422998.1	GI:22317418			
KEYWORDS					
SOURCE		Candida albicans.			
ORGANISM		Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.			
FEATURES		1			
REFERENCE					
AUTHORS					
TITLE		Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.			
JOURNAL		Gene disruption methodologies for drug target discovery			
FEATURES		1. (bases 1 to 24)			
source		Patent: WO 2005328-A 298 11-JUN-2002; Elitra Pharmaceuticals Inc. (US)			
BASE COUNT	17 a	17 a	8 c	9 g	31 t
ORIGIN					
Query Match		0.5%; Score 17; DB 6; Length 65;			
Best Local Similarity		100.0%; Pred. No. 2.5e+03;			
Matches		17; Conservative 0; Mismatches 0;			
Indels		0; Gaps 0;			
Qy	2567	TTCCTCTCTCTCTCTCT	2583		
Db	2	TTCCTCTCTCTCTCTCT	18		
RESULT 12					
REFERENCE					
AUTHORS					
LOCUS	E225574	E225574	24 bp	RNA	linear
DEFINITION		RNA molecule inhibiting hepatitis C virus NS3 protease.			PAT 18-JUN-2001
ACCESSION	E225574				
VERSION	E225574	GI:13024842			
KEYWORDS					
SOURCE		Unidentified.			
ORGANISM		unclassified.			
FEATURES		1. (bases 1 to 24)			
REFERENCE					
AUTHORS					
LOCUS	Satoshi,N., Pemmecha,K. and Kotaro,F.	Satoshi,N., Pemmecha,K. and Kotaro,F.	24 bp	DNA	linear
DEFINITION		RNA molecule inhibiting hepatitis C virus NS3 protease.			PAT 18-JUN-2001
ACCESSION	E225575				
VERSION	E225576.1	GI:13024842			
KEYWORDS					
SOURCE		Unidentified.			
ORGANISM		unclassified.			
FEATURES		1. (bases 1 to 24)			
REFERENCE					
AUTHORS					
LOCUS	PI/SATOSHI/NISHIKAWA, PEMMECHA, KUMARU, KOTARO, FUKUDA, PC	PI/SATOSHI/NISHIKAWA, PEMMECHA, KUMARU, KOTARO, FUKUDA, PC	24 bp	RNA	linear
DEFINITION		C12N15/09, A61K31/70, A61K31/70, C12N15/00			PAT 07-NOV-1997
ACCESSION	C12N15/09				
VERSION	C12N15/09				
KEYWORDS					
SOURCE		Strandedness: Single;			
ORGANISM		Topology: Linear;			
FEATURES		1. .24			
source		Key: Location; Location/Qualifiers			
BASE COUNT	12 a	12 a	0 c	12 g	0 t
ORIGIN					

Search completed: January 11, 2003, 06:03:29
 Job time : 9360 secs

Query Match 0.4%; Score 16; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2217 TCTCCTCTTCTTC 2232
 Db 17 TCTCCTCTTC 2

RESULT 14

AX042974 AX042974
 LOCUS AX042974
 DEFINITION Sequence 540 from Patent WO0065088.
 ACCESSION AX042974
 VERSION AX042974.1 GI:11341582
 KEYWORDS synthetic construct.
 SOURCE ORGANISM synthetic construct.
 ARTIFICIAL SEQUENCES.
 REFERENCE 1 (bases 1 to 25)

AUTHORS Ulfendahl, P.J. and Wong, K.C.
 TITLE Primers for identifying typing or classifying nucleic acids
 JOURNAL Patent: WO 0065088-A 540 02-NOV-2000;
 Amersham Pharmacia Biotech AB (SE)
 Location/Qualifiers 1..25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="16S rRNA Homozygote Primer Sequence"

BASE COUNT 4 a 2 c 5 g 14 t
 ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2577 TTTTTTTCTGAAA 2592
 Db 3 TTTTTTTCTGAAA 18

RESULT 15

AX043091 AX043091
 LOCUS AX043091
 DEFINITION Sequence 657 from Patent WO0065088.
 ACCESSION AX043091
 VERSION AX043091.1 GI:11341699

KEYWORDS synthetic construct.
 SOURCE ORGANISM synthetic construct.
 ARTIFICIAL SEQUENCES.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Ulfendahl, P.J. and Wong, K.C.
 TITLE Primers for identifying typing or classifying nucleic acids
 JOURNAL Patent: WO 0065088-A 657 02-NOV-2000;
 Amersham Pharmacia Biotech AB (SE)
 Location/Qualifiers 1..25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="16S rRNA Homozygote Primer Sequence"

BASE COUNT 2 a 5 c 2 g 16 t
 ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 TTTTTTTTCAGATGT 83
 Db 4 TTTTTTTCAGATGT 19

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